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(FILE 'HOME' ENTERED AT 10:32:42 ON 17 JAN 2005)

FILE 'DISSABS, 1MOBILITY, AGRICOLA, AQUASCI, BIOTECHNO, COMPENDEX,  
COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, MEDICONF,  
OCEAN, PAPERCHEM2, PASCAL, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT,  
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COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, MEDICONF,  
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ON 17 JAN 2005

E KATO-SEISHI?/AU  
E KATO SEISHI?/AU

L1        258 S E2  
            E KIMURA-TOMOKO?/AU  
            E KIMURA TOMOKO?/AU  
L2        222 S E2  
L3        6 S HP03380  
L4        21 S L1 AND L2

[0335] Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 4B.

TABLE 4B

Comparison of NOV4a against NOV4b and NOV4c.		
Protein Sequence	NOV4a Residues/ Match Residues	Identities/Similarities for the Matched Region
NOV4b	1 ... 305	270/305 (88%)
	1 ... 305	273/305 (88%)
NOV4c	1 ... 305	272/318(85%)
	1 ... 318	274/318 (85%)

[0336] Further analysis of the NOV4a protein yielded the following properties shown in Table 4C.

TABLE 4C

Protein Sequence Properties NOV4a	
PSort analysis:	0.8200 probability located in outside; 0.5246 probability located in lysosome (lumen); 0.1783 probability located in microbody (peroxisome); 0.1000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	Cleavage site between residues 31 and 32

[0337] A search of the NOV4a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 4D.

TABLE 4D

Geneseq Results for NOV4a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV4a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE05186	Human drug metabolising enzyme (DME-17) protein - <i>Homo sapiens</i> , 210 aa. [WO200151638-A2, 19 JUL. 2001]	1 ... 210 1 ... 210	210/210 (100%) 210/210 (100%)	e-123
AAU29291	Human PRO polypeptide sequence #268 - <i>Homo sapiens</i> , 210 aa. [WO200168848-A2, 20 SEP. 2001]	1 ... 210 1 ... 210	210/210 (100%) 210/210 (100%)	e-123
AAB42269	Human ORFX ORF2033 polypeptide sequence SEQ ID NO: 4066 - <i>Homo sapiens</i> , 210 aa. [WO200058473-A2, 05 OCT. 2000]	1 ... 210 1 ... 210	205/210 (97%) 208/210 (98%)	e-120
AAB75350	Human secreted protein #9 - <i>Homo sapiens</i> , 302 aa. [WO200100806-A2, 04 JAN. 2001]	63 ... 302 58 ... 299	120/242 (49%) 168/242 (68%)	1e-70
AAB61614	Human protein HP03380 - <i>Homo sapiens</i> , 302 aa. [WO200102563-A2, 11 JAN. 2001]	63 ... 302 58 ... 299	120/242 (49%) 168/242 (68%)	1e-70

[0338] In a BLAST search of public sequence databases, the NOV4a protein was found to have homology to the proteins shown in the BLASTP data in Table 4E.

TABLE 4E

Public BLASTP Results for NOV4a					
Protein Accession Number	Protein/Organism/Length	NOV4a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value	
Q64686	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase III (EC 2.4.99.-) (ST6GalNAc III) (Sialyltransferase 7C) (STY) - <i>Rattus norvegicus</i> (Rat), 305 aa.	1 ... 305 1 ... 305	253/305 (82%) 277/305 (89%)	e-158	
Q9WUV2	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase (EC 2.4.99.-) (ST6GALNACIII) - <i>Mus musculus</i> (Mouse), 305 aa.	1 ... 305 1 ... 305	251/305 (82%) 275/305 (89%)	e-156	

## WEST Search History

DATE: Monday, January 17, 2005

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
<i>DB=EPAB; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L9	WO-200102563-A2.did.	0
<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L8	200102563.pn.	7
<input type="checkbox"/>	L7	HP03380	1
<input type="checkbox"/>	L6	L5	8
<input type="checkbox"/>	L5	L4 and l3	8
<input type="checkbox"/>	L4	Kimura-Tomoko.in.	42
<input type="checkbox"/>	L3	Kato-seishi.in.	60
<input type="checkbox"/>	L2	Kato-seishi.in.6639063.pn.	0
<i>DB=USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L1	6639063.pn.	1

END OF SEARCH HISTORY